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(54) **METHOD OF MULTIPLEX LIGASE CHAIN REACTION**

VERFAHREN ZUR MEHRFACHEN LIGASE-KETTENREAKTION

PROCEDE DE REACTION DE LIGASE EN CHAINE MULTIPLEX

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Description**Background:**

[0001] This application relates to amplification of DNA and, in particular, to the simultaneous amplification of multiple target sequences using the Ligase Chain Reaction (hereinafter "LCR").

[0002] This application is related to several other applications relating to LCR, including EP 320 308 and EP 439 182.

[0003] LCR is a method for amplifying exponentially the number of detectable target molecules. It involves the use of two pairs of probes. A first or primary pair hybridizes with one strand of a target sequence at near-adjacent positions so that they can be ligated together in template-dependent fashion to form a reorganized primary molecule. The secondary pair is capable of hybridizing to the reorganized primary molecule. LCR was first described by Backman, et al. in EP-A-320 308. Much has been written about it since then. For example, see Wallace, EP-A-336 731; Orgel, WO 89/09835; Richards, WO 89/12696; Segev, WO 90/01069; and Barany, *Proc. Natl Acad Sci USA* 88:189-193 (1991). A variation of LCR known as "Gap" LCR is described in EP-A-439 182 and in Segev, WO 90/01069.

[0004] Instead of using two pairs of probes capable of forming blunt-ended duplexes, at least one probe of one of the probe pairs initially includes a "modified" end which renders the resultant duplex "nonblunt" and/or not a suitable substrate for the ligase catalyzed fusion of the two probe duplexes. A "modified end" has either (1) a blocking moiety (or additional base residues) on a group (e.g. the 5' phosphate or the 3' hydroxyl) which, under ordinary LCR conditions, obligatorily participates in the ligase catalyzed fusion or (2) omitted bases to create a "gap" between one probe terminus and the next probe terminus.

[0005] In the "gap" embodiment, modified ends are created by eliminating from one or more of the probes a short sequence of bases, thereby leaving a recess or gap between the 5' end of one probe and the 3' end of the other probe when they are both hybridized to the target (or target complement, or polynucleotide generated therefrom). In order for LCR to amplify the target, the gaps between the probes must be filled in (i.e., the modification must be "corrected"). In a first version, this can be done using a polymerase or a reverse transcriptase and an excess of deoxynucleotide triphosphates which are complementary to the target strand opposite the gap. Alternatively, this can be done by supplying a fifth probe complementary to the target and a sixth probe complementary to the fifth probe.

[0006] PCR or polymerase chain reaction is a different method for amplifying DNA. It employs two primers which hybridize to opposite strands of a double stranded target. A polymerase initiates extension of the primer using the target as a template by sequentially adding the appropriate complementary nucleotides. PCR is described in U.S. Patents 4,883,195 and 4,883,202.

[0007] PCR has been used in a multiplex manner to determine the presence of multiple target sequences in a single reaction. EP-A-364 255 describes the use of multiple primer sets to simultaneously amplify multiple target sequences by PCR. A similar disclosure is made in Chamberlain, et al., *Nucl. Acids Res.*, 16:1141-56 (1988).

[0008] In addition, Nickerson, et al., *Proc. Natl. Acad. Sci. USA*, 87:8923-8927 (1990) proposes an oligonucleotide ligation assay ("OLA") for multiple target sequences, pending the development of "multiple, nonisotopic reporter groups". OLA employs two contiguous probes that are ligated together and the ligated product is detected as a measure of the presence of a target sequence.

[0009] In spite of the existence of these disclosures, multiplex LCR is not available in the hands of the public. The art does not provide sufficient guidance actually to enable the concept of multiplex LCR. This is due largely to the inapplicability of PCR conditions to LCR.

Summary of the Invention:

[0010] Accordingly, we have now demonstrated the feasibility of multiplex LCR with as many as seven different probe sets. In one aspect, the invention is a method for performing LCR amplification simultaneously on two or more target sequences. The method comprises the steps of:

- a. providing a reaction solution containing nucleic acid of a sample as single-stranded nucleic acid, said sample putatively having one or more of a plurality of target nucleic acid sequences;
- b. for each putative target sequence, providing in the reaction solution at least four nucleic acid probes (a probe set), wherein: i) the first and second of said probes are primary probes, and the third and fourth of said probes are secondary nucleic acid probes; ii) the first probe is a single strand capable of hybridizing to a first segment of a primary strand of the target nucleic acid; iii) the second probe is a single strand capable of hybridizing to a second segment of said primary strand of the target nucleic acid; iv) the 5' end of the first segment of said primary strand of the target is positioned relative to the 3' end of the second segment of said primary strand of the target to enable joining of the first probe to the second probe when said probes are hybridized to said primary strand of said target

nucleic acid, thus forming a reorganized primary molecule having a first portion and a second portion; v) the third probe is capable of hybridizing to a first portion of the reorganized primary molecule; and vi) the fourth probe is capable of hybridizing to a second portion of the reorganized primary molecule, the first portion of the reorganized primary molecule being positioned relative to the second portion of the reorganized primary molecule to enable joining of the third probe to the fourth probe when said third and fourth probes are hybridized to said reorganized primary molecule, thus forming a reorganized secondary molecule; and wherein for each putative target sequence said probe set is provided at a concentration that enables said joining in the presence of each of the other probe sets; and

c. repeating the following cycle:

- i) hybridizing said probes with nucleic acid in said sample;
- ii) performing said joining to form said reorganized molecules; and
- iii) denaturing nucleic acid in said sample;

whereby with successive cycles the quantity of reorganized primary and secondary molecules is increased for each putative target sequence present in the reaction solution.

[0011] In the usual case, the joining is performed by a ligase enzyme, or a ligase enzyme and a polymerase enzyme. Usually, the cycle of step c is repeated from 10 to 100 times, preferably from 20 to about 60 times.

[0012] Generally, the amplification product is detected by means of a unique detectable label associated with each probe set, each of said detectable labels being differentiable from the others. Labels preferably include specific binding members, such as haptens or polynucleotides. The labels can be used for either detection, or separation or both. In a preferred configuration, each of the probe sets are labeled with two distinct labels such that the reorganized molecules, when hybridized together, are labeled with two labels, at least one of which is a unique label and the other label is a common label, the same for each probe set.

[0013] In a preferred protocol, the common label is used for detection and the unique label is used to separate the reorganized molecules of one probe set from the reorganized molecules of at least one other probe set. Separation may be accomplished by different binding locations on a single solid phase, or by using a solid phase which is characterized by a property which permits differentiation of one from another.

[0014] In a second aspect, the invention is a method of detecting the presence, absence or quantity of each of a plurality of target nucleic acid sequences by a multiplex ligase chain reaction comprising the steps of:

a. providing a reaction solution containing nucleic acid of a sample as single-stranded nucleic acid, said sample putatively having one or more of a plurality of target nucleic acid sequences;

b. for each putative target sequence, providing in the reaction solution a set of at least two and optionally four nucleic acid probes (a probe set), wherein: i) the first and second of said probes are primary probes, and the optional third and fourth of said probes are secondary nucleic acid probes; ii) the first probe is a single strand capable of hybridizing to a first segment of a primary strand of the target nucleic acid; iii) the second probe is a single strand capable of hybridizing to a second segment of said primary strand of the target nucleic acid; iv) the 5' end of the first segment of said primary strand of the target is positioned relative to the 3' end of the second segment of said primary strand of the target to enable joining of the first probe to the second probe when said probes are hybridized to said primary strand of said target nucleic acid, thus forming a reorganized primary molecule having a first portion and a second portion; v) the third probe is capable of hybridizing to a first portion of the reorganized primary molecule; and vi) the fourth probe is capable of hybridizing to a second portion of the reorganized primary molecule, the first portion of the reorganized primary molecule being positioned relative to the second portion of the reorganized primary molecule to enable joining the third probe to the fourth probe when said third and fourth probes are hybridized to said reorganized primary molecule, thus forming a reorganized secondary molecule; wherein at least one probe of each probe set contains a detectable label, the detectable label associated with each probe set being differentiable from the detectable labels associated with the other probe sets, whereby the presence, absence or quantity of each putative target sequence can be determined; and wherein for each putative target sequence said probe set is provided at a concentration that enables said joining in the presence of each of the other probe sets; and

c. performing the following cycle:

- i) hybridizing said probes with nucleic acid in said sample;
- ii) performing said joining to form said reorganized molecules; and
- iii) denaturing nucleic acid in said sample;

whereby with each cycle the quantity of reorganized primary and, optionally, secondary molecules is increased for each putative target sequence present in the reaction solution; and

d. measuring the detectable label associated with each of said probe sets as a measure of the presence or quantity of target nucleic acid in the reaction solution.

[0015] The same variations of labeling, separation and detection mentioned above are useful for this aspect of the invention.

[0016] Finally, the invention relates to an immunochromatographic device and method for multiplex detection of multiple analytes. The device comprises a strip of porous material capable of transporting fluids by capillary action, said strip having at least first and second unique capture reagents immobilized thereon in first and second discrete spots spaced apart from an end used to contact transport fluid, said unique first and second capture reagents being specific different first and second analytes, respectively, wherein said second discrete spot is spaced from said first discrete spot in both vertical and horizontal dimensions, vertical being the direction of fluid flow. Preferably, the device contains three or more discrete spots, and said spots are all spaced from one another in both vertical and horizontal dimensions to form a substantially linear, diagonal array of spots.

[0017] The method of using the device involves contacting said contact end with a test solution suspected to contain the analyte under conditions that allow said solution to be transported by capillary action at least to the most distal capture spot; and determining for each capture spot, whether analyte became bound to said capture spot.

[0018] The method and device are useful for conventional specific binding analytes, such as antigens and antibodies, as well as for polynucleotide analytes.

Brief Description of the Drawings:

[0019]

Fig 1 is a diagram of the immunochromatography strip used in multiplex LCR detection.

Figs 2a and 2b are photographs showing the immunochromatographic strip results of multiplex LCR performed on patient samples from example 7

Fig 3 is a photograph showing the immunochromatographic strip results of multiplex LCR performed on patient samples from example 10.

Detailed Description:

[0020] As used in this application, a "multiplex" process refers to the carrying out of a method or process simultaneously and in the same reaction vessel on two or more, typically three or more, different target sequences. Thus, multiplex LCR is the performance of LCR on a plurality of targets using at least one set of four probes for each putative target sequence. In like manner, the term "N-plex" LCR, where N is a numeral, refers to LCR performed to amplify or detect one or more of N target sequences.

[0021] A "target sequence" or "target nucleic acid" is a segment of nucleic acid (DNA or RNA) The segment may be from about 10 or 15 to several hundred nucleotides in length. For LCR, a target segment is usually about 30 to about 60 nucleotides and the sequence is known. A target is "putative" if its presence is expected or anticipated, or if it or a variation of it is expected or anticipated. For example, in multiplex LCR of a homozygote to determine which of two mutually exclusive alleles is present, the sequences surrounding both alleles are putative target sequences, even though it is known that only one is expected to be present The possible alternatives for each allele are all putative targets.

[0022] The step of "joining" as recited above encompasses several known methods of joining two probes together. The preferred method is by the use of a thermostable ligase, although other ligases and other ligating agents are not excluded. Ligases are discussed in the incorporated EP-A-320 308 and in EP-A-373 962.

[0023] Joining is also possible by chemical means or by photoligation. Joining also encompasses the possible intermediate step of "correcting" a modified end as taught in

[0024] EP-A-439 182. Correction includes the filling of a gap with an extending reagent (such as polymerase) as well as the cleaving of a blocking group (such as with endonuclease IV).

[0025] A reaction solution is typically prepared by collecting the sample from a patient and disrupting the cells to release the DNA or RNA. Detergents may be used, but other known methods of sample preparation are also included. Specific buffer compositions are available from the literature, and from the examples. The DNA or RNA is rendered single-stranded by altering the stringency conditions, usually by heating.

[0026] The probes for multiplex LCR are generally no different than the probes for conventional LCR. However, to facilitate detection at least one probe of each probe set should bear a detectable label. Moreover, the detectable labels

from each of the probe sets must all be differentiable, one from the other, either by signal differentiation or by spatial differentiation. As is described in more detail below, signal differentiation refers to the ability to distinguish targets in essentially the same location (i.e. homogeneous assay) by virtue of differences in the signal (e.g. different fluorescent emission wavelengths or different colors). By contrast, spatial differentiation refers to the ability to distinguish targets based on the position or location of the signal. Spatial differentiation is also known as separation and may be accomplished by size, molecular weight, charge density, or magnetic or specific binding properties, and the like. Of course, it is possible and often desirable to utilize both types of differentiation within the same system.

[0027] Where separation is preferred in order to interpret the results, a preferred embodiment uses two labels: at least one of which is a unique or differentiable label. The other label may be common, and shared by each of the probe sets, or it may be unique as well. Depending on the particular protocol used (see below), either the common label or the unique label may be used for detection, and the other label may be used for separation.

[0028] The term "label" refers to a molecule or moiety having a property or characteristic which is capable of detection. A label may be directly detectable, as with radioisotopes, fluorophores or chemilumiphores; or a label may be indirectly detectable, as with haptens or polynucleotide tails. When indirect labels are used for detection or signalling purposes, they are used in conjunction with a signalling entity complex. A "signalling entity" is a molecule or moiety which provides the detectable property or characteristic. The signalling entity may be direct, as with a colloidal particle (e.g. colloidal gold or selenium); or it may be indirect, as with an enzyme (e.g. alkaline phosphatase, β -galactosidase or horseradish peroxidase). Indirect signalling entities may require additional components, e.g. substrate, as is well known in the art. The "signalling entity complex" includes a signalling entity conjugated to specific binding partner, such as an antibody or polynucleotide. Such conjugates may be prepared according to any known method of conjugation.

[0029] Useful labels include radioisotopes, especially as the common label. However, it may be possible to use a radioisotope as a unique label when the radiation can be differentiated. Likewise, fluorophores and chemilumiphores are best used as common labels, although it would be possible to use them as unique labels if their signal can be differentiated (e.g. on the basis of wavelength). A hapten, polynucleotide or other specific binding member may also serve as the common label, although the ability to easily distinguish one specific binding member from another renders them ideally suited for the unique label. When different specific binding members are employed, conjugates bearing different specific binding partners are used according to one of the protocols described below.

[0030] Many different haptens are known, and virtually any hapten can be used with the present invention. The invention requires only that a specific binding partner is known or can be prepared (a definitional property of "hapten") and that the hapten can be coupled to the probe such that it does not interfere with hybridization. Many methods of adding haptens to probes are known in the literature. Enzo Biochemical (New York) and Clontech (Palo Alto) both have described and commercialized probe labelling techniques. For example, a primary amine can be attached to a 3' oligo end using 3'-Amine-ON CPG™ (Clontech, Palo Alto, CA). Similarly, a primary amine can be attached to a 5' oligo end using Aminomodifier II® (Clontech). The amines can be reacted to various haptens using conventional activation and linking chemistries.

[0031] In addition, WO92/10505 and U.S. 5,290,925 teach methods for labelling probes at their 5' and 3' ends respectively. Both the aforementioned co-pending applications are incorporated by reference. Some illustrative haptens include many drugs (eg. digoxin, theophylline, phencyclidine (PCP), salicylate, etc.), T3, biotin, fluorescein (FITC), dansyl, 2,4-dinitrophenol (DNP); and modified nucleotides such as bromouracil and bases modified by incorporation of a N-acetyl-7-iodo-2-fluorenylamino (AIF) group; as well as many others. Certain haptens described herein are disclosed in U.S. 5,424,414 (adamantaneacetic acids), U.S. 5,464,746 (carbazoles and dibenzofurans), WO93/20074 (acridines), and WO93/20094 (quinolines), (collectively referred to herein as the "hapten applications").

[0032] It should be understood that the number of probes necessary for multiplex amplification or detection is generally four times the number of putative sequences. In the case of an assay for "N" different bacterial organisms, the number of probes required is $4 \times N$. In the case of genetic testing of mutations, the rule of $4 \times T$ probes, where T is the number of putative targets, is still the general or usual case. However, certain exceptions are described below. It should be kept in mind that, depending on the type and complexity of the mutation, there may be several putative targets for each mutation. Take for example, a simple, single base substitution. If it is known that the substitution is always one type of base, the possible putative target sequences are two: the wild type and the mutation substitution. However, if it is known that any of the four bases can substitute at the locus, then the putative target sequences become four. The general rule requires eight ($4 \times T$, $T=2$) probes in the first case; and 16 ($4 \times T$, $T=4$) probes in the second.

[0033] The general rule of four probes for each putative target will hold regardless of the type and complexity of the mutation. However, in some simple mutations two probes from one set (say, arbitrarily, the right two) will also serve as the two (right) probes from the other sets and fewer than $4 \times T$ probes will be required. These simple mutations include any small deletion, insertion or substitution the ends of which are known with certainty. So long as the ends are known, the size of the deletion, insertion or change does not affect its characterization as "simple". With these "simple" mutations, the number of probes required is $(2T+2)$. The +2 is the common probe set on one side of the mutation, while the 2T represents all the possible permutations of the mutation, i.e. all the possible putative target sequences. Of course,

the number of possible permutations depends on the nature of the mutation.

[0034] Another "special case" where less than 4T probes are required is possible where the mutation configuration of the gene is such that two mutations are near enough to one another that a common probe can be used between the two mutations, with specialized probes on the outside ends. "Near enough" in this context means within a distance that can be spanned by an LCR probe. Typically, that distance is about 20 to 40 bases.

[0035] Interpretation of LCR results may include looking at the number of cycles required to produce target and background curves that are distinguishable from one another. For a given concentration of probes, the background signal will develop after n cycles, while the target signal develops after only t cycles. In order for LCR to be useful as a diagnostic tool, it is desired that n be far greater than t ; i.e. that there be as large a "cycle window" as possible between target and background. see, e.g. EP-A-320 308. It has also been shown that the cycle number at which signal "comes up" varies with probe concentration: The higher the probe concentration, the sooner the signal comes up, and vice versa. As a consequence, it has been discovered that it is preferable to balance the probe concentration carefully in multiplex LCR. Since all reactions are run for the same number of cycles, all target signals must "come up" at approximately the same time. This can be insured by carefully balancing the concentration of each probe set so that each reaction reaches peak or at least detectable signal levels at approximately the same cycle number. It is impossible to predict precisely how to adjust probe concentration for a given probe set, but this can readily be determined empirically through simple experiments.

[0036] It is generally known that the melt temperature of the probe sets for LCR should be approximately equal. However, it has been discovered in multiplex LCR that the melt temperatures may vary by as much as 8 to 10° C from one side to the other.

[0037] Other reaction conditions for multiplex LCR are similar to those used for more fundamental LCR. The same buffer, pH and salt conditions are generally acceptable. However, it is desirable to add a somewhat higher concentration of ligase, as shown in the examples. In addition, if gap filling LCR is used, additional polymerase may be desired as well.

[0038] As mentioned above, the most preferred protocols include two labels, a common label and a unique label. Either may serve as the detection label. For simplicity, the embodiments are described using haptens as both the common and unique labels. It is, of course, understood that another label is easily substituted for at least one of the haptens, especially the common hapten.

[0039] According to a preferred standard LCR protocol, a first hapten is used to capture and separate the reorganized molecules. A second hapten is used to couple the reorganized complex with the signalling entity. This procedure is described more completely in EP-A-439 182. For example a fluorescein moiety is attached to the 5' end of the first primary probe and to the 3' end of the first secondary probe. In addition, a different hapten, say biotin, is attached to the 3' end of the second primary probe and to the 5' end of the second secondary probe. Thus, when the reorganized molecules are duplexed, two biotins are found at one end of the duplex and two fluoresceins are found at the other end. A solid phase having a coating of anti-fluorescein is used to separate reorganized molecules from unligated probes having biotins. (Unligated probes having fluoresceins are also captured.) The separated complexes are detected by using avidin or anti-biotin labeled with a detectable signalling entity such as an enzyme.

[0040] For multiplex LCR this system of separation and detection need only be slightly modified. It is still possible to use just one hapten common to all probe sets at one end (detection or capture) of the reorganized molecules. Only the other end of the molecules needs to be differentiable, e.g. via a unique hapten. Two distinct protocols are possible.

[0041] First, the common hapten (say, biotin) could be used to capture all the reorganized molecules. Then the different complexes can be differentiated by using specific haptens, and anti-hapten conjugates with differentiable signalling entities. For example (paying attention to the orientation and proper probe end considerations mentioned above) probes for target A are labeled with biotin and fluorescein; probes for target B are labeled with biotin and dansyl; and probes for target C are labeled with biotin and digoxin. All reorganized molecules (and biotinylated probes) are captured on a solid phase. Anti-fluorescein coupled to colloidal gold produces a reddish brown color if target A is present, anti-dansyl coupled to colloidal selenium produces a pinkish color if target B is present and anti-digoxin coupled to polypyrrole latex produces a black color if target C is present. As an alternative, the antibodies can be coupled to different enzymes (eg. alkaline phosphatase, peroxidase, β -galactosidase) the substrates or products of which produce different colors.

[0042] Since discerning different colors on a single solid phase may be difficult, a second and more preferred protocol involves using the common hapten/label as the detection function and using the unique hapten to separate the targets from one another on one or more solid phases. For example, beads or microparticles which can be physically separated (eg. by manipulation, filtration, chromatography, sedimentation, centrifugation, magnetic field, etc.) may be used as a solid phase. Separable groups of these solid phases are each coated with antibody against one of the unique haptens. After multiplex LCR and incubation with the solid phases, the groups are separated and a common signalling entity complex is reacted with the common hapten. Different sequences are determined by the appearance of signal on one or more of the different solid phase groups.

[0043] A dot-blot method is also useful to separate reorganized molecules. To discrete locations on a sheet-like

solid phase are immobilized antibodies to the several unique haptens. Incubation of this sheet with the reaction solution will permit separation of the reorganized molecules, based on the specificity of the antibodies for the unique haptens. Again, the common hapten is employed with a signalling entity conjugate to generate signal at any location which contains a reorganized molecule. The solid phase is interpreted based on the location (and optionally the intensity) of the signal.

[0044] A variation of this technique employs immunochromatography to separate the reorganized molecules on the basis of the unique hapten. Rather than incubate the solid phase with the reaction solution, the solid phase is a porous chromatographic material and the reaction solution wicks through it, drawn by capillary action. A preferred porous material is nitrocellulose. As with the dot-blot method, antibody to each unique hapten is immobilized at various locations throughout the snip, preferably along a diagonal line. When the reaction solution carrying all the reorganized molecules encounters an immobilized antibody spot, the reorganized molecules bearing the complementary hapten are "captured" and immobilized at that location. This technique is a variation of the technique described in EP-A-357 011.

[0045] It has been found that the immunochromatography method works best when the capture spots for various polynucleotide targets (and even regular analytes) are aligned in a diagonal configuration as shown in Figure 1. It is desirable to spatially separate capture spots in both dimensions for several reasons. First, vertical separation is useful to better differentiate signals from adjacent spots. However, if the spots are spaced only in this dimension, there is a tendency for label to accumulate at the first positive capture spot. Spots downstream from this spot are "shadowed" and generally do not develop signal as readily. Thus, it is preferred to separate spots in a horizontal direction as well. Spots spaced only in a horizontal direction would require a much wider snip in order to achieve the resolution necessary to read the snip.

[0046] In yet another variation of either protocol the reorganized molecules can be separated and/or detected by sequence-specific probe hybridization instead of haptens. This variation is possible with the separable groups of solid phases, with the sheet-like solid phase and with the chromatographic medium. The only difference is that, instead of immobilizing a unique hapten-specific antibody on the solid phase, a hybridization probe is immobilized, the probe being specific for sequences found in the first primary and or first secondary probes (ie. the same probes which carried the unique hapten in the prior variation). The method of chromatographic medium specific hybridization is described further in EP-A-387 696.

[0047] The multiplex LCR method of the present invention has numerous applications, depending on the type of target employed. First, it is useful in genetic screening or testing. Often a particular genetic disease or trait manifests itself as a mutation or change in the genetic code at one or a finite number of locations in the genome. Some diseases or conditions (e.g. sickle cell anemia, phenylketonuria, Tay-Sachs disease, medium chain acyl CoA dehydrogenase deficiency, cystic fibrosis) manifest themselves as a point mutation of a single base in the DNA. Others (e.g. cystic fibrosis, Duchene's Muscular Dystrophy (DMD)) can manifest themselves by short alterations or deletions in one or a relatively small number of exon locations. The ability to do multiplex LCR permits the simultaneous analysis of an individual's DNA at each of the exons where deletions/alterations are known to be causative for a particular disease.

[0048] Another use for multiplex LCR is in the diagnosis of certain bacterial or viral diseases which typically occur from many variant strains of an infecting organism or virus. For example, human papilloma virus (HPV) types 6, 8, 11, 16, 18, 31, and 33 are all known to exist. Universal or consensus probes and primers will amplify all HPV regardless of type. However, only types 16, 18 and possibly 33 are of significant clinical interest due to their association with cancerous lesions. Thus, a multiplex LCR assay permits the simultaneous type-specific amplification of each variant. This gives the clinician additional information not available from simple universal amplification or from simple type-specific amplification of one type. This approach is also useful for HIV, which has at least two known types; and for *Chlamydia trachomatis*, which has at least 15 serovars.

[0049] It may also be useful to perform multiplex LCR when only a single organism is of interest. For example, multiple target sequences may be picked for confirmation or improved specificity. For example, sequences from both the MOMP gene and the cryptic plasmid might be selected to detect *C. trachomatis* DNA. Alternatively, internal controls might be run by including probes that will amplify β -globin sequences, as well as probes that will amplify the desired target.

[0050] Another use for multiplex LCR is in identity testing. A panel of perhaps 10 or more sequences may be selected which are highly variant in the general population. By determining the presence or absence of each of these sequences, an individual may be "typed" with a unique pattern of presence or absence of each particular exon sequence. In a binary format, individual "A" is identified as "0111001001", while individual "B" is identified as "0000111011", where a "0" indicates the absence of a particular exon sequence and a "1" indicates the presence of a particular exon sequence.

[0051] Other uses will be readily apparent to those skilled in this art.

EXAMPLES

[0052] The invention will be more completely understood with reference to the following examples which are intended to be illustrative only, and do not limit the invention. Throughout the examples the following abbreviations have the meanings given.

- BSA refers to bovine serum albumin.
- EPPS refers to a buffer of N-(2-hydroxyethyl)piperazine-N'-(3-propanesulfonic acid).
- NAD refers to nicotinamide adenine dinucleotide, an energy source for certain biological reactions.
- PCR refers to the polymerase chain reaction
- TRIS refers to *tris*- (hydroxymethyl)aminomethane buffer
- TTP refers to thymidine triphosphate, one of the substrates for polymerase.
- Abbott TestPack Plus™ is a trademark of Abbott Laboratories used to designate a chromatographic or wicking type of immunoassay. This assay format is described in further detail in EP-A- 421 294 and EP-A-357 011, as well as in other literature.

Example 1: Oligo Synthesis and Haptenation

Part A - Sequence and Synthesis:

[0053] The following oligonucleotides (see Table 1) were synthesized following established procedures using β -cyanoethylphosphoramidites on a model 380A DNA synthesizer (Applied Biosystems, Foster City CA), where x = primary amine derived from 3'-Amine-ON CPG™ (Clontech, Palo Alto, CA), y = primary amine derived from Arninomodifier II® (Clontech), p = phosphate derived from Phosphate-ON® (Clontech), and A,C,G, and T have their usual meanings. Probes are written 5' to 3' from left to right. Melting temperatures are given for probe pairs as follows: first and second hybridize, and third and fourth hybridize.

Table 1

Sequence ID No	SEQUENCE	Melt Temp (°C)	DMD Exon No.
1. 2. 3. 4.	yCACTGCGGGT TTTGCAGAAC AATAA pATTGTTCTGC AAAACCCGCA GT-thiophene carbazole pGTAAGTAGTA CCCTGGACAA GGTx yGACCTTGTCC AGGGTACTAC TTACA		4
5. 6. 7. 8.	CAAGTTTTGC CTCAACAAGT GAGCA pGCTCACTTGT TGAGGCAAAA CTT-dansyl pGAAGCCATCC AGGAAGTGGA AAx yATTTCCACTT CCTGGATGGC TTCAA		8
9. 10. 11. 12.	yTACATCCTTC TCAATGTCCA ATAGA pCTATTGGACA TTGAGAAGGA TGT-quinoline pGCCCCCAAAT GCGAACATTC CATx yTATGGAATGT TCGCATTGTT GGGCA		12
13. 14. 15. 16.	yACAGGCTGTC ACCACCACTC AGCCA pGGCTGAGTGG TGGTGACAGC CTA-quinoline pCACTAACACA GACAAGTGT ATGx yCCATTACAGT TGTCTGTGTT AGTGA	74° 66°	17
17. 18. 19. 20.	yCGTGATAAGC TGACAGAGTG AAACA pGTTTCACTCT GTCAGCTTAT CACG-dibenzofuran pGTTAAGGCTT GAAAGGGCAA GTAGx yCTACTTGCCC TTTCAAGCCT TAACA	69° 68°	19
21. 22. 23. 24.	yTTTTACCTGC AGGCGATTG ACAGA pCTGTCAAATC GCCTGCAGGT AAx pCTGTTGAGAA ATGGCGGCGT TTTx yGAAAACGCCG CCATTTCTCA ACAGA		44
25. 26. 27. 28.	yTTGAATGCAA CTGGGGAAGA AATAA pATTTCTTCCC CAGTTGCATT CA-dansyl pCAGCAATCCT CAAAAACAGA TGAx yGCATCTGTTT TTGAGGATTG CTGAA	66° 67°	45

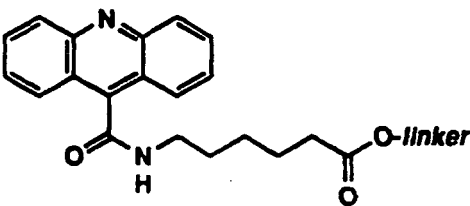
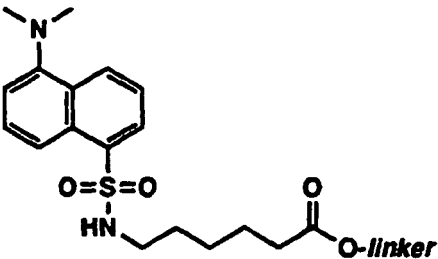
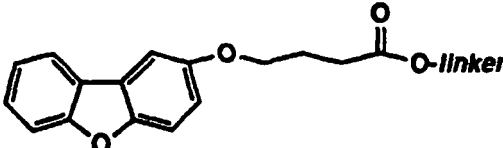
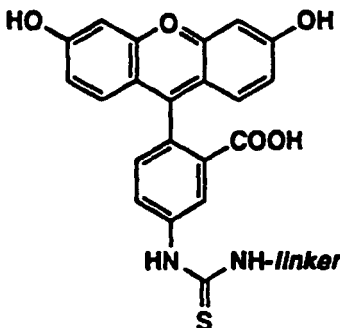
29.	yAAGACCTTGA	AGAGCAGTTA	AATCA		
30.	pGATTTAACTG	CTCTTCAAGG	TCT-thiophene carbazole		48
31.	pCTGCTGCTGT	GGTTATCTCC	TATx		
32.	yAATAGGAGAT	AACCACAGCA	GCAGA		
33.	yCAAGTTATAA	AATCACAGAG	GGTGA		
34.	pCACCCCTCTGT	GATTTTATAA	CTTx	65'	51
35.	pGGTGGGTGAC	CTTGAGGATA	TCAx		
36.	yTTGATATCCT	CAAGGTCACC	CACCA	70'	
37.	acridine-CCTGTGGGGC	AAGGTGAACG	TGGA		
38.	pCCACGTTTCAC	CTTGCCCCAC	AG-acridine		human β
39.	pGAAGTTGGTG	GTGAGGCCCT	GGx		globin
40.	yCCCAGGGCCT	CACCACCAAC	TTCA		gene

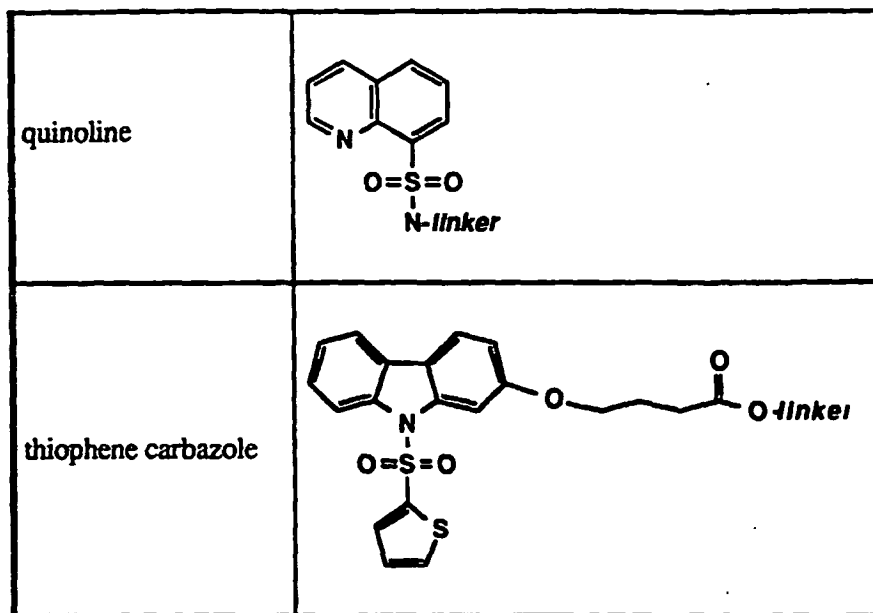
[0054] Oligos 1-4 are specific for a portion of exon 4 of the Duchenne Muscular Dystrophy (DMD) gene, following the numbering scheme described by Koenig M, Monaco AP, and Kunkel, LM. in *The complete sequence of dystrophin predicts a rod shaped cytoskeletal protein*. *Cell* 53, 219-228 (1988). According to the same numbering scheme, oligos 5-8 are specific for a portion of exon 8 of the Duchenne Muscular Dystrophy gene; oligos 9-12 are specific for a portion of exon 12 of the DMD gene; oligos 13-16 are specific for a portion of exon 17 of the DMD gene; oligos 17-20 are specific for a portion of exon 19 of the DMD gene; oligos 21-24 are specific for a portion of exon 44 of the DMD gene; oligos 25-28 are specific for a portion of exon 45 of the DMD gene; oligos 29-32 are specific for a portion of exon 48 of the DMD gene; and oligos 33-36 are specific for a portion of exon 51 of the DMD gene. Oligos 37-40 are specific for a portion of the human β -globin gene and are used as a control.

Part B - Haptenation

[0055] The 3'-end of some oligonucleotides were conjugated with haptens, as indicated in Table 1. The conjugation of these haptens followed standard β -cyanoethyl-phosphoramidite chemistry, and is described in the aforementioned hapten applications. A similar procedure is described for fluorescent label conjugates in published U.S. application NTIS ORDER No. PAT-APPL-7-246,688 (Cohen, et al., 1989). The structures of the haptens used are shown in Table 2, below:

Table 2

Hapten	Structure
acridine	
dansyl	
dibenzofuran	
fluorescein	



[0056] All oligonucleotides were purified by reversed-phase HPLC to remove failure sequences and, in the case of haptenated oligos, any unhaptenated species.

Example 2: Biotinylation

[0057] The aminated ends of oligos 3, 4, 7, 8, 11, 12, 15, 16, 19, 20, 23, 24, 27, 28, 31, 32, 35, 36, 39, and 40 from example 1 were labeled with biotin essentially following the protocol of Urdea, *et. al.*, *Nuci. Acids Res.*, **16(11)**:4937-4956 (1988). Briefly, up to 1 mg oligo was dissolved in 100 μ L of 0.1 M sodium phosphate buffer, pH 7.5, and treated with 2 mg biotin-(aminocaproyl)2-N-hydroxysuccinimide ester in 100 μ L dimethylformamide (DMF) for 16 hours at room temperature.

[0058] Oligos 22 (3' end) and 33 (5' end) were linked to fluorescein after synthesis by dissolving up to 1 mg oligo in 100 μ L of 0.1 M sodium borate buffer, pH 9.0, and treating with 2 mg of fluorescein isothiocyanate (FITC) for 15 hours at room temperature. Alternatively, the 3' aminated end of oligo 34 could be reacted with FITC, rather than haptenating oligo 33.

[0059] All biotin- and fluorescein-labeled oligonucleotides were purified by column chromatography through Sephadex[®] G-25 (Pharmacia, Piscataway NJ), preparative gel electrophoresis, and ethanol precipitation.

[0060] For quality control purposes, the integrity of reorganized molecules after performing LCR was monitored on the IMx[®] instrument (Abbott Labs) using the typical biotin/fluorescein bihaptenated complex as taught in EP-A-439 182. For this reason, oligos 1, 9, 13, 17, 21, 25 and 29 were synthesized with a 5' primary amine. Portions of these oligos were reacted with fluorescein, as above, to provide the biotin/fluorescein complex necessary for IMx analysis. However, when used in multiplex LCR, the unhaptenated, aminated oligos were used.

Example 3: LCR Reaction Conditions

[0061] The labeled oligos of example 2 were used, in various combinations, in "gap filling" modified LCR essentially as described in EP-A-439 182. In general, the following reagents were mixed in a 0.5 mL polypropylene tube:

Reagent	Final Concentration
water	(to give a final volume of 45 μ L)

(continued)

Reagent	Final Concentration
reaction buffer	15 mM EPPS pH 7.8 20 mM KCl 30 mM MgCl ₂
oligonucleotides	see Table 3
NAD	0.1 mM
TTP	1 μ M
sample	250 ng DNA
mineral oil	2 drops/tube

[0062] The mixture was heated at 100°C for 3 minutes, cooled, and the following were added in a volume of 5 μ L, to give a final reaction volume of 50 μ L:

Reagent	Final Concentration
DNA ligase from <i>Thermus thermophilus</i>	3400 U/50 μ L
DNA polymerase from <i>Thermus</i> (MBR Inc., Milwaukee WI)	1.2 U/50 μ L

[0063] The mixture was then subjected to 37 cycles of programmed temperature change, the cycle being 85°C for 30 seconds and 45°C for 20 seconds. The thermal cycling was carried out in a TempCycler™ (Coy Laboratory Products, Ann Arbor MI).

Table 3

To Detect This Exon	Use These Oligos	At These Concentrations (number of molecules of each oligo per reaction tube (50 μ L))
Exon 4	1-4	1.5×10^{12}
Exon 8	5-8	7.7×10^{11}
Exon 12	9-12	3.8×10^{11}
Exon 17	13-16	7.7×10^{11}
Exon 19	17-20	7.7×10^{11}
Exon 44	21-24	3.8×10^{11}
Exon 45	25-28	3.8×10^{11}
Exon 48	29-32	3.1×10^{11}
Exon 51	33-36	3.8×10^{11}
β -globin	37-40	7.7×10^{11}

Example 4: Antibodies and Solid Phase

[0064] Antiserum was raised in rabbits against immunogens prepared from conjugates of hapten and either bovine serum albumin (BSA) or keyhole limpet hemocyanin (KLH). The preparation and description of these sera is described in the above-mentioned hapten applications, although any known procedure for raising antibodies would suffice. These sera were purified by passage through protein A Sepharose® (Pharmacia).

[0065] Antiserum against dansyl was a mouse monoclonal obtained from the University of Pennsylvania (Fan, S-T. and Karush, F. *Molecular Immunology* 21:1023-1029 (1984)).

[0066] These antisera were diluted in 0.1 M TRIS pH 7.8, 0.9% NaCl, 0.1% BSA, 1% sucrose, and a trace of phenol red. Portions (0.2 μ L) of these diluted antisera were spotted in a regular pattern (see Figure 1) onto strips of nitrocellulose (Schleicher and Schuell AE 98, 5 μ m) of dimensions approximately 4 x 50 mm. The concentrations of antisera were as indicated in Table 4.

Table 4

antiserum against	concentration (mg/mL)
acridine	2.55
dansyl	0.5
dibenzofuran	3.4
fluorescein	0.5
quinoline	0.75
thiophene carbazole	0.25

Example 5: Label Conjugate

[0067] Colloidal selenium was prepared following the procedure of Yost, D.A. *et. al.* (U.S. patent 4,954,452 (1990)). The colloid was diluted in water to achieve an optical density of 16 at 545 nm. To 1 mL of this suspension was added 1 μ L of antibiotin (Abbott Laboratories) at 1 mg/mL and 60 μ L of BSA at 100 mg/mL. This mixture was mixed on a vortex mixer for 1 minute.

Example 6: Multiplex Immunochromatography

[0068] The LCR reaction mixtures of Example 3 were analyzed by Abbott TestPack Plus™ immunochromatography essentially following the protocol of EP-A-357 011. Briefly, the colloidal suspension of Example 5 (15 μ L) was diluted with buffer (14 μ L; 0.1 M TRIS pH 7.8, 0.9% NaCl, 3% alkali-treated casein) and mixed with the product of the LCR reaction (1 μ L). A nitrocellulose strip of Example 4 was admitted to the suspension. After 5 minutes, the chromatography process was complete, and the nitrocellulose strip was removed from the reaction/colloid suspension and allowed to dry. The presence of a colored spot at the locus of antibody application indicated the presence of a specific LCR product.

Example 7: Analysis of Patient Samples for DMD

[0069] Samples of human DNA obtained from patients with Duchenne Muscular Dystrophy were analyzed for the presence of exons 4, 12, 17, 19, 44, 45, 48, and 51 using oligos 1-4 and 9-36. Oligos 37-40 were included in the reaction mix as a procedural control to detect the presence of human DNA. The analysis of each sample was performed in two parts: in one reaction tube was the mixture described in Example 3 containing oligos 13-28 and 33-40 (to amplify exons 17, 19, 45, 48, and 51; along with human β -globin); and in another tube was the LCR reaction mix containing oligos 1-4, 9-12, 29-32, and 37-40 (to amplify exons 4, 12, and 44; along with human β -globin). These analyses were performed by subjecting the sample DNA to LCR following Example 3, and subsequently immunochromatography of the resulting mix following Example 6.

[0070] In Figure 2 are shown photographs of nitrocellulose strips after immunochromatography. The photograph of Figure 2a shows 7 nitrocellulose strips. These show the presence of amplification products specific for (spots from bottom to top) human β -globin, and DMD exons 17, 45, 48, 51, and 19. The samples contained 250 ng of DNA from, respectively (from left to right): salmon sperm DNA; 5 individual patients suffering from Duchenne Muscular Dystrophy (patient numbers indicated in the photograph), and normal human DNA. Similarly, the photograph of Figure 2b shows 5 nitrocellulose strips. These show the presence of amplification products specific for (spots from bottom to top) human β -globin, and DMD exons 12, 4, and 44. The samples contained 250 ng of DNA from, respectively (from left to right): salmon sperm DNA; 3 individual patients suffering from Duchenne Muscular Dystrophy (patient numbers not indicated in the photograph—these are (from left to right) patients 5294, 4036, and 638), and normal human DNA.

[0071] The missing exons for each patient are known from PCR (see Table 5).

Table 5

Patient Number	Exons Deleted (by PCR) <i>all others will be amplified</i>
4722	17, 19, 45, 48, and 51 (44 not tested)
5294	4, 12, 17 and 19
5303	45
5396	51
638	4, 12, 17, 19, 44, and 45
4036	12 and 44 (17, 19, 45, 48, and 51 not tested)

Example 8: Oligo Synthesis for cystic fibrosis

[0072] The following oligonucleotides (see Table 6) were synthesized following established procedures using β -cyanoethylphosphoramidites on a model 380A DNA synthesizer (Applied Biosystems, Foster City CA), where p = phosphate derived from Phosphate-ON[®] (Clontech), biotin is introduced using Biotin-ON[®] (Clontech), and A,C,G, and T have their usual meanings. Probes are written 5' to 3' from left to right. Haptentation as indicated was performed as described in Example 1.

Table 6

Sequence ID No.	SEQUENCE	CF mutation
41. 42. 43. 44.	Dansyl-GTGAATCAC ACTGAGTGA GA pTCTCCACTCA GTGTGATTCC AC pTCAACGAGCA AGAATTTCTT T-biotin biotin-AAAGAAATTC TTGCTCGTTG A	G551D
45. 46. 47. 48.	biotin-ATTCAATAAC TTTGCAACAG TG pCACTGTTGCA AAGTTATTGA AT-biotin pAAGGAAAGCC TTTGGAGT thioph.-carb.-ACTCCAAAGG CTTTCCTT	W1282X
49. 50. 51. 52.	fluorescein-GGCACCATTA AAGAAAATAT CAT pATGATATTTT CTTTAATGGT GCC pTGGTGTTC TATGATGAAT ATA-biotin biotin-TATATTCATC ATAGGAAACA CCA	Δ F508

Example 9: LCR Reaction Conditions

[0073] The labeled oligos of example 8 were used for blunt LCR essentially as described in EP-A-320-308 using the following concentrations of reagents:

Reagent	Final Concentration
water	(to give a final volume of 45 μ L)
reaction buffer	50 mM EPPS pH 7.8 150 mM KCl 10 mM MgCl ₂
oligonucleotides 41, 42, 43, and 44	3.3x10 ¹¹ copies of each
oligonucleotides 45, 46, 47, and 48	4.2x10 ¹¹ copies of each
oligonucleotides 49, 50, 51, and 52	2.7x10 ¹¹ copies of each
NAD	0.1 mM
BSA	5 μ g
sample	250 ng DNA
mineral oil	2 drops/tube

[0074] The mixtures were heated at 100°C for 3 minutes, cooled to room temperature, and the following were added in a volume of 5 μ L:

Reagent	Final Concentration
DNA ligase from <i>Thermus thermophilus</i>	3400 U/50 μ L

[0075] The mixture was then subjected to 45 cycles of programmed temperature change, this cycle being 85°C for 30 seconds and 57°C for 20 seconds. The thermal cycling was carried out in a TempCycler™ (Coy Laboratory Products, Ann Arbor MI).

Example 10: Analysis of Patient Samples for cystic fibrosis mutations

[0076] Samples of human DNA obtained from patients with Cystic Fibrosis were analyzed for the presence of mutations G551D, W1282X, and Δ F508 using oligos 41-52. These analyses were performed by subjecting the sample DNA to LCR following Example 9, and subsequent immunochromatography of the resulting mix following Example 6. Reagents were prepared as before (see Examples 4-6).

[0077] In Figure 3 is shown a photograph of nitrocellulose strips after immunochromatography. It shows the presence of amplification products specific for (spots from bottom and left to top and right) CF mutations W1282X, Δ F508, and G551D. The samples were: 1) water (no DNA), 2) patient heterozygous for G542X mutation, 3) patient heterozygous for W1282X mutation, 4) patient heterozygous for Δ F508 mutation, and 5) patient heterozygous for G551D mutation. No spot appears after amplification of water or G542X DNA (strips 1 and 2). Only one spot appears on strip 3, and this is located near the left of the strip (locus of *anti*-thiophene-carbazole immobilization), indicating a positive amplification of only the W1282X DNA. Only one spot appears on strip 4, and this is near the middle of the strip (locus of *anti*-fluorescein immobilization), indicating a positive amplification of only Δ F508 DNA. Only one spot appears on strip 5, and this is located near the right of the strip (locus of *anti*-dansyl immobilization), indicating a positive amplification of only G551D DNA.

[0078] Although all 12 oligos were present in all the reaction tubes, permitting the amplification of DNA from all three mutations, only the specific DNA present in each sample actually was amplified. Each patient was heterozygous for their particular mutation, meaning that each also carried one normal gene. In no case was the normal gene shown

to be amplified by any of the oligonucleotides.

SEQUENCE LISTING

5

(1) GENERAL INFORMATION:

10

(i) APPLICANT: ABBOTT LABORATORIES and:
Bouma, Stanley R.
Gordon, Julian
Hoijer, Joannel
Jou, Cynthia
Rhoads, James

15

(ii) TITLE OF INVENTION: METHOD OF MULTIPLEX LIGASE CHAIN
REACTION

(iii) NUMBER OF SEQUENCES: 52

20

(iv) CORRESPONDENCE ADDRESS:

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(D) STATE: Illinois
(E) COUNTRY: U.S.
(F) ZIP: 60064-3500

25

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Rel #1.0, Ver #1.25 /WordPerfect

30

(vii) PRIOR APPLICATION DATA:

(A) DOCUMENT NUMBER: 07/860,702
(B) COUNTRY: U.S.
(C) FILING DATE: 31 March 1992

35

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(B) REGISTRATION NUMBER: 32,459
(C) REFERENCE/DOCKET NUMBER: 5155.PC.01

40

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (708) 937-4884

45

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50

55

(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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(2) INFORMATION FOR SEQ ID NO:2:

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 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 22
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATTGTTCTGC AAAACCCGCA GT

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
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 (B) LOCATION: 23
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTAAGTAGTA CCCTGGACAA GGT

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GACCTTGTC AGGGTACTAC TTACA

(2) INFORMATION FOR SEQ ID NO:5:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
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 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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15 (2) INFORMATION FOR SEQ ID NO:6:

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 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 23
25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCTCACTTGT TGAGGCAAAA CTT

23

30 (2) INFORMATION FOR SEQ ID NO:7:

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 (B) TYPE: nucleic acid
35 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 22
40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAAGCCATCC AGGAAGTGGA AA

22

45 (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
50 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:

55

(A) NAME/KEY: misc_feature

(B) LOCATION: 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATTTCCTT CCTGGATGGC TTCAA

25

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TACATCCTTC TCAATGTCCA ATAGA

25

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTATTGGACA TTGAGAAGGA TGT

23

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCCCCCAAAT GCGAACATTC CAT

23

(2) INFORMATION FOR SEQ ID NO:12:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
10 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

15 TATGGAATGT TCGCATTGG GGGCA

25

 (2) INFORMATION FOR SEQ ID NO:13:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
25 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

30 ACAGGCTGTC ACCACCACTC AGCCA

25

 (2) INFORMATION FOR SEQ ID NO:14:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
40 (A) NAME/KEY: misc_feature
 (B) LOCATION: 23
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

45 GGCTGAGTGG TGGTGACAGC CTA

23

 (2) INFORMATION FOR SEQ ID NO:15:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
50 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)

55

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CACTAACACA GACAACTGTA ATG

23

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCATTACAGT TGTCTGTGTT AGTGA

25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGTGATAAGC TGACAGAGTG AAACA

25

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTTTCACTCT GTCAGCTTAT CACG

24

(2) INFORMATION FOR SEQ ID NO:19:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
10 (ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 24
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

15 GTTAAGGCTT GAAAGGGCAA GTAG 24

(2) INFORMATION FOR SEQ ID NO:20:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
25 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

30 CTACTTGCCC TTTCAAGCCT TAACA 25

(2) INFORMATION FOR SEQ ID NO:21:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
40 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

45 TTTTACCTGC AGGCGATTG ACAGA 25

(2) INFORMATION FOR SEQ ID NO:22:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 23
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTGTCAAATC GCCTGCAGGT AAA

23

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 23
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTGTTGAGAA ATGGCGGCGT TTT

23

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAAAACGCCG CCATTCTCA ACAGA

25

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTGAATGCAA CTGGGAAGA AATAA

25

(2) INFORMATION FOR SEQ ID NO:26:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
10 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 22
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

15 ATTTCTTCCC CAGTTGCATT CA 22

(2) INFORMATION FOR SEQ ID NO:27:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
25 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 23
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

30 CAGCAATCCT CAAAACAGA TGA 23

(2) INFORMATION FOR SEQ ID NO:28:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
40 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

45 GCATCTGTTT TTGAGGATTG CTGAA 25

(2) INFORMATION FOR SEQ ID NO:29:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

55

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAGACCTTGA AGAGCAGTTA AATCA

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 23
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATTAACTG CTCTTCAAGG TCT

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 23
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTGCTGCTGT GGTATCTCC TAT

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AATAGGAGAT AACCACAGCA GCAGA

25

5

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc_feature

15

(B) LOCATION: 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CAAGTTATAA AATCACAGAG GGTGA

25

20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

25

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc_feature

30

(B) LOCATION: 23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CACCTCTGT GATTTTATAA CTT

23

35

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

40

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc_feature

45

(B) LOCATION: 23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGTGGGTGAC CTTGAGGATA TCA

23

50

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

55

5 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

10

TTGATATCCT CAAGGTCACC CACCA

25

(2) INFORMATION FOR SEQ ID NO:37:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
20 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

25

CCTGTGGGGC AAGGTGAACG TGGA

24

(2) INFORMATION FOR SEQ ID NO:38:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
35 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 22
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

40

CCACGTTCAC CTTGCCCCAC AG

22

(2) INFORMATION FOR SEQ ID NO:39:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
50 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 22
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

55

GAAGTTGGTG GTGAGGCCCT GG

22

5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

15

(A) NAME/KEY: misc_feature

(B) LOCATION: 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCCAGGGCCT CACCACCAAC TTCA

24

20

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

25

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

30

(A) NAME/KEY: misc_feature

(B) LOCATION: 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTGGAATCAC ACTGAGTGGA GA

22

35

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

40

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCTCCACTCA GTGTGATTCC AC

22

45

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

50

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
5 (A) NAME/KEY: misc_feature
(B) LOCATION: 21
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TCAACGAGCA AGAATTCTT T

21

10 (2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: misc_feature
20 (B) LOCATION: 1
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

AAAGAAATTC TTGCTCGTTG A

21

25 (2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: misc_feature
35 (B) LOCATION: 1
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATTCAATAAC TTGCAACAG TG

22

40 (2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
45 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: misc_feature
50 (B) LOCATION: 22
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CACTGTTGCA AAGTTATTGA AT

22

(2) INFORMATION FOR SEQ ID NO:47:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
10 (ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AAGGAAAGCC TTTGGAGT

18

15 (2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
20 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1
25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACTCCAAAGG CTTTCCTT

18

30 (2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1
40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGCACCATTA AAGAAAATAT CAT

23

45 (2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
50 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

55

ATGATATTTT CTTTAATGGT GCC

23

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TGGTGTTTCC TATGATGAAT ATA

23

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TATATTCATC ATAGGAAACA CCA

23

Claims

1. A method of performing multiplex ligase chain reaction comprising the steps of:

a. providing a reaction solution containing nucleic acid of a sample as single-stranded nucleic acid, said sample putatively having one or more of a plurality of target nucleic acid sequences;

b. for each putative target sequence, providing in the reaction solution at least four nucleic acid probes (a probe set), wherein: i) the first and second of said probes are primary probes, and the third and fourth of said probes are secondary nucleic acid probes; ii) the first probe is a single strand that hybridizes to a first segment of a primary strand of the target nucleic acid iii) the second probe is a single strand that hybridizes to a second segment of said primary strand of the target nucleic acid; iv) the 5' end of the first segment of said primary strand of the target is positioned relative to the 3' end of the second segment of said primary strand of the target to enable joining of the first probe to the second probe when said probes are hybridized to said primary strand of said target nucleic acid, thus forming a reorganized primary molecule having a first portion and a second portion; v) the third probe hybridizes to a first portion of the reorganized primary molecule; and vi) the fourth probe hybridizes to a second portion of the reorganized primary molecule, the first portion of the reorganized primary molecule being positioned relative to the second portion of the reorganized primary molecule to enable joining of the third probe to the fourth probe when said third and fourth probes are hybridized to said reorganized primary molecule, thus forming a reorganized secondary molecule; and

wherein for each putative target sequence said probe set is balanced such that each probe set is provided at a concentration that enables said joining in the presence of each of the other probe sets; and

wherein each probe set produces a detectable product after the same number of amplification cycles; and
c. repeating the following cycle:

- i) hybridizing said probes with nucleic acid in said sample;
- ii) performing said joining to form said reorganized molecules; and
- iii) denaturing nucleic acid in said sample;

whereby with successive cycles the quantity of reorganized primary and secondary molecules is increased for each putative target sequence present in the reaction solution.

2. The method according to claim 1, wherein said joining is performed by a ligase enzyme, or a ligase enzyme and a polymerase enzyme.
3. The method according to claim 1, wherein the cycle of step c is repeated from 20 to about 60 times.
4. The method according to claim 1, wherein at least one probe from each probe set carries a detectable label, each of said detectable labels being differentiable from the others.
5. The method according to claim 4, wherein said detectable labels comprise haptens which are differentiable based on the specificity of different specific binding members.
6. The method according to claim 1, wherein each of the probe sets are labeled with two distinct labels such that the reorganized molecules, when hybridized together, are labeled with two labels, at least one of which is a unique label that is different for each of the probe sets.
7. The method according to claim 6, wherein the other label is a common label, the same for each probe set.
8. The method according to claim 7, wherein the common label is used for detection and is selected from the group consisting of radioisotopes, fluorophores, chemilumiphores and haptens.
9. The method according to claim 6, wherein the unique labels comprise unique specific binding members such that each unique specific binding member is differentiable from every other specific binding member.
10. The method according to claim 9, wherein the unique labels comprise specific haptens.
11. The method according to claim 9, wherein the unique labels comprise specific hybridization probes.
12. The method according to claim 9, wherein the unique specific binding member is used to separate the reorganized molecules of one probe set from the reorganized molecules of at least one other probe set.
13. The method according to claim 12, wherein the separation is achieved by immobilizing a specific binding partner for each specific binding member at a different location on a solid phase.
14. The method according to claim 12, wherein the separation is achieved by immobilizing a specific binding partner for each specific binding member on a solid phase, said solid phase being characterized by a property which permits differentiation of one from another.
15. A method of detecting the presence, absence or quantity of each of a plurality of target nucleic acid sequences by a multiplex ligase chain reaction comprising the steps of:

- a. providing a reaction solution containing nucleic acid of a sample as single-stranded nucleic acid, said sample putatively having one or more of a plurality of target nucleic acid sequences;
- b. for each putative target sequence, providing in the reaction solution a set of at least two and optionally four nucleic acid probes (a probe set), wherein: i) the first and second of said probes are primary probes, and the optional third and fourth of said probes are secondary nucleic acid probes; ii) the first probe is a single strand that hybridizes to a first segment of a primary strand of the target nucleic acid, iii) the second probe is a single strand that hybridizes to a second segment of said primary strand of the target nucleic acid; iv) the 5' end of the first segment of said primary strand of the target is positioned relative to the 3' end of the second segment

of said primary strand of the target to enable joining of the first probe to the second probe when said probes are hybridized to said primary strand of said target nucleic acid, thus forming a reorganized primary molecule having a first portion and a second portion; v) the third probe hybridizes to a first portion of the reorganized primary molecule; and vi) the fourth probe hybridizes to a second portion of the reorganized primary molecule, the first portion of the reorganized primary molecule being positioned relative to the second portion of the reorganized primary molecule to enable joining the third probe to the fourth probe when said third and fourth probes are hybridized to said reorganized primary molecule, thus forming a reorganized secondary molecule; wherein at least one probe of each probe set contains a detectable label, the detectable label associated with each probe set being differentiable from the detectable labels associated with the other probe sets, whereby the presence, absence or quantity of each putative target sequence can be determined: and wherein for each putative target sequence said probe set is balanced such that each probe set is provided at a concentration that enables said joining in the presence of each of the other probe sets; and wherein each probe set produces a detectable product after the same number of amplification cycles; and c. performing the following cycle:

- i) hybridizing said probes with nucleic acid in said sample;
- ii) performing said joining to form said reorganized molecules; and
- iii) denaturing nucleic acid in said sample;

whereby with each cycle the quantity of reorganized primary and, optionally, secondary molecules is increased for each putative target sequence present in the reaction solution; and d. measuring the detectable label associated with each of said probe sets as a measure of the presence or quantity of target nucleic acid in the reaction solution.

16. The method according to claim 15, wherein said joining is performed by a ligase enzyme, or a ligase enzyme and a polymerase enzyme.

17. The method according to claim 15, wherein said third and fourth probes are provided and the cycle of step c is repeated from 10 to about 100 times.

18. The method according to claim 15, wherein the cycle of step c is repeated from 20 to about 60 times.

19. The method according to claim 15, wherein the probes are labeled with two labels such that the reorganized molecules are labeled with two labels, at least one of which is a unique label that is different for each of the probe sets.

20. The method according to claim 17, wherein the probes are labeled with two labels such that the reorganized molecules are labeled with two labels, at least one of which is a unique label that is different for each of the probe sets and the other of which is a common label.

21. The method according to claim 20, wherein the common label is used for detection and is selected from the group consisting of radioisotopes, fluorophores, chemilumiphores and haptens.

22. The method according to claim 20, wherein the unique labels comprise haptens and wherein each unique hapten differs from every other unique hapten.

23. The method according to claim 20, wherein the unique labels comprise specific hybridization probes.

24. The method according to claim 22, wherein the unique hapten is used to separate the different reorganized molecules.

25. The method according to claim 24, wherein the separation is achieved by immobilizing a specific binding partner for each unique hapten at a different location on a solid phase.

26. The method according to claim 24, wherein the separation is achieved by immobilizing a specific binding partner for each unique hapten on a solid phase, said solid phase being characterized by a property which permits differentiation of one from another

Patentansprüche

1. Verfahren zur Durchführung von Multiplex-Ligase-Kettenreaktion, das folgende Schritte umfaßt:

- 5 a. die Bereitstellung einer Reaktionslösung, die die Nukleinsäure einer Probe als einzelsträngige Nukleinsäure enthält, wobei die Probe vermutlich eine oder mehrere einer Vielzahl von TargetNukleinsäuresequenzen enthält;
- 10 b. die Bereitstellung von mindestens vier Nukleinsäuresonden (ein SONDENSATZ) in der Reaktionslösung für jede vermutliche Targetsequenz, worin i) die erste und zweite Sonde Primärsonden sind, und die dritte und vierte Sonde sekundäre Nukleinsäuresonden sind; ii) die erste Sonde ein Einzelstrang ist, der an ein erstes Segment eines Primärstrangs der Targetnukleinsäure hybridisiert; iii) die zweite Sonde ein Einzelstrang ist, der an ein zweites Segment des Primärstrangs der Targetnukleinsäure hybridisiert; (iv) das 5'-Ende des ersten Segments des Target-Primärstrangs bezüglich des 3'-Endes des zweiten Segments des Target-Primärstrangs positioniert ist, um die Verbindung der ersten Sonde mit der zweiten Sonde zu ermöglichen, wenn die Sonden an den Primärstrang der Targetnukleinsäure hybridisiert sind, wodurch ein reorganisiertes Primärmolekül gebildet wird, das aus einem ersten Abschnitt und einen zweiten Abschnitt besteht; v) die dritte Sonde an einen ersten Abschnitt des reorganisierten Primärmoleküls hybridisiert; und vi) die vierte Sonde an einen zweiten Abschnitt des reorganisierten Primärmoleküls hybridisiert, wobei der erste Abschnitt des reorganisierten Primärmoleküls bezüglich des zweiten Abschnitts des reorganisierten Primärmoleküls positioniert ist, um die Verbindung der dritten Sonde mit der vierten Sonde zu ermöglichen, wenn die dritte und vierte Sonde an das reorganisierte Primärmolekül hybridisiert sind, wodurch ein reorganisiertes Sekundärmolekül gebildet wird; und
- 15 worin für jede vermutliche Targetsequenz der SONDENSATZ so abgeglichen ist, dass jeder SONDENSATZ bei einer Konzentration bereitgestellt wird, die die Verbindung in Gegenwart aller anderen SONDENSATZE ermöglicht; und worin jeder SONDENSATZ ein nachweisbares Produkt nach der gleichen Zahl von Amplifikationszyklen produziert; und
- 20 c. die Wiederholung des folgenden Zyklus:
 - 30 i) die Hybridisierung der Sonden mit der Nukleinsäure in der Probe;
 - ii) die Vornahme der Verbindung, um reorganisierte Moleküle zu bilden, und
 - iii) das Denaturieren von Nukleinsäure in der Probe;
- 35 wobei mit zunehmender Zykluszahl die Menge reorganisierter Primär- und Sekundärmoleküle für jede vermutliche Targetsequenz, die in der Reaktionslösung vorhanden ist, zunimmt.
2. Verfahren nach Anspruch 1, worin die Verbindung über ein Ligaseenzym, oder über ein Ligaseenzym und ein Polymeraseenzym vorgenommen wird.
- 40 3. Verfahren nach Anspruch 1, worin der Zyklus von Schritt c 20 bis etwa 60 mal wiederholt wird.
4. Verfahren nach Anspruch 1, worin mindestens eine Sonde jedes SONDENSATZES einen nachweisbaren Marker trägt und jeder nachweisbare Marker jeweils von den anderen unterscheidbar ist.
- 45 5. Verfahren nach Anspruch 4, worin die nachweisbaren Marker Haptene enthalten, die auf der Basis der Spezifität verschiedener spezifischer Bindungsglieder unterscheidbar sind.
6. Verfahren nach Anspruch 1, worin jeder SONDENSATZ mit zwei unterschiedlichen Markern gekennzeichnet ist, so dass die reorganisierten Moleküle, wenn sie zusammen hybridisiert sind, mit zwei Markern gekennzeichnet sind, von denen mindestens einer ein eindeutiger Marker ist, der für jeden SONDENSATZ verschieden ist.
- 50 7. Verfahren nach Anspruch 6, worin der andere Marker ein allgemeiner Marker ist, der gleiche für jeden SONDENSATZ.
8. Verfahren nach Anspruch 7, worin der allgemeine Marker für den Nachweis verwendet wird und gewählt ist aus der Gruppe, die aus Radioisotopen, Fluorophoren, Chemilumiphoren und Haptenen besteht.
- 55 9. Verfahren nach Anspruch 6, worin die eindeutigen Marker eindeutige spezifische Bindungsglieder enthalten, so

dass jedes spezifische Bindungsglied von jedem anderen spezifischen Bindungsglied unterscheidbar ist.

10. Verfahren nach Anspruch 9, worin die eindeutigen Marker spezifische Haptene enthalten.

11. Verfahren nach Anspruch 9, worin die eindeutigen Marker spezifische Hybridisierungs sonden enthalten.

12. Verfahren nach Anspruch 9, worin das eindeutige spezifische Bindungsglied verwendet wird, um die reorganisierten Moleküle eines SONDENSATZES von den reorganisierten Molekülen mindestens eines anderen SONDENSATZES zu trennen.

13. Verfahren nach Anspruch 12, worin die Trennung erreicht wird, indem ein spezifischer Bindungspartner für jedes spezifische Bindungsglied an einer unterschiedlichen Stelle auf einer festen Phase immobilisiert wird.

14. Verfahren nach Anspruch 12, worin die Trennung erreicht wird, indem ein spezifischer Bindungspartner für jedes spezifische Bindungsglied auf einer festen Phase immobilisiert wird, und die feste Phase durch eine Eigenschaft charakterisiert ist, die die Unterscheidung voneinander gestattet.

15. Verfahren für den Nachweis des Vorhandenseins, des Fehlens oder der Menge jeder einzelnen einer Vielzahl von Targetnukleinsäuresequenzen durch eine Multiplex-Ligase-Kettenreaktion, das die folgenden Schritte umfaßt:

a. die Bereitstellung einer Reaktionslösung, die die Nukleinsäure einer Probe als einzelsträngige Nukleinsäure enthält, wobei die Probe vermutlich eine oder mehrere einer Vielzahl von Targetnukleinsäuresequenzen enthält;

b. die Bereitstellung in der Reaktionslösung eines Satzes von mindestens zwei und wahlweise vier Nukleinsäuresonden (ein SONDENSATZ) für jede vermutliche Targetsequenz, worin i) die erste und zweite der Sonden Primärsonden sind, und die wahlweise dritte und vierte Sonde sekundäre Nukleinsäuresonden sind; ii) die erste Sonde ein Einzelstrang ist, der an ein erstes Segment eines Primärstrangs der Targetnukleinsäure hybridisiert; iii) die zweite Sonde ein Einzelstrang ist, der an ein zweites Segment des Primärstrangs der Targetnukleinsäure hybridisiert; (iv) das 5'-Ende des ersten Segments des Target-Primärstrangs bezüglich des 3'-Endes des zweiten Segments des Target-Primärstrangs positioniert ist, um die Verbindung der ersten Sonde mit der zweiten Sonde zu ermöglichen, wenn die Sonden an den Primärstrang der Targetnukleinsäure hybridisiert sind, wodurch ein reorganisiertes Primärmolekül gebildet wird, das aus einem ersten Abschnitt und einem zweiten Abschnitt besteht; v) die dritte Sonde an einen ersten Abschnitt des reorganisierten Primärmoleküls hybridisiert; und vi) die vierte Sonde an einen zweiten Abschnitt des reorganisierten Primärmoleküls hybridisiert, wobei der erste Abschnitt des reorganisierten Primärmoleküls bezüglich des zweiten Abschnitts des reorganisierten Primärmoleküls positioniert ist, um die Verbindung der dritten Sonde mit der vierten Sonde zu ermöglichen, wenn die dritte und vierte Sonde an das reorganisierte Primärmolekül hybridisiert sind, wodurch ein reorganisiertes Sekundärmolekül gebildet wird;

worin mindestens eine Sonde jedes SONDENSATZES einen nachweisbaren Marker enthält, und der nachweisbare Marker, der jedem SONDENSATZ zugeordnet ist, unterscheidbar ist von den nachweisbaren Markern, die den anderen SONDENSATZEN zugeordnet sind, wobei das Vorhandensein, das Fehlen oder die Menge jeder vermutlichen Targetsequenz bestimmt werden kann; und worin für jede vermutliche Targetsequenz der SONDENSATZ so abgeglichen ist, dass jeder SONDENSATZ bei einer Konzentration bereitgestellt wird, die die Verbindung in Gegenwart aller anderen SONDENSATZE ermöglicht; und
worin jeder SONDENSATZ ein nachweisbares Produkt nach der gleichen Zahl von Amplifikationszyklen produziert; und

c. die Durchführung des folgenden Zyklus:

- i) das Hybridisieren der Sonden mit der Nukleinsäure in der Probe;
- ii) das Vornehmen der Verbindung, um die reorganisierten Moleküle zu bilden, und
- iii) das Denaturieren von Nukleinsäure in der Probe;

wobei mit jedem Zyklus die Menge reorganisierter Primär- und, wahlweise, Sekundärmoleküle für jede vermutliche Targetsequenz, die in der Reaktionslösung vorhanden ist, vergrößert wird; und

d. das Messen des nachweisbaren Markers, der jedem SONDENSATZ zugeordnet ist, als Maß für das Vorhan-

densein oder die Menge an Targetnukleinsäure in der Reaktionslösung.

16. Verfahren nach Anspruch 15, worin die Verbindung über ein Ligaseenzym, oder über ein Ligaseenzym und ein Polymeraseenzym vorgenommen wird.
17. Verfahren nach Anspruch 15, worin die dritte und vierte Sonde bereitgestellt werden und der Zyklus von Schritt c 10 bis etwa 100 mal wiederholt wird.
18. Verfahren nach Anspruch 15, worin der Zyklus von Schritt c 20 bis etwa 60 mal wiederholt wird.
19. Verfahren nach Anspruch 15, worin die Sonden mit zwei Markern gekennzeichnet sind, so dass die reorganisierten Moleküle mit zwei Markern gekennzeichnet sind, von denen mindestens einer ein eindeutiger Marker ist, der für jeden SONDENSATZ verschieden ist.
20. Verfahren nach Anspruch 17, worin die Sonden mit zwei Markern gekennzeichnet sind, so dass die reorganisierten Moleküle mit zwei Markern gekennzeichnet sind, von denen mindestens einer ein eindeutiger Marker ist, der für jeden SONDENSATZ verschieden ist, und der andere ein allgemeiner Marker ist.
21. Verfahren nach Anspruch 20, worin der allgemeine Marker für den Nachweis verwendet wird und gewählt ist aus der Gruppe, die aus Radioisotopen, Fluorophoren, Chemilumiphoren und Haptenen besteht.
22. Verfahren nach Anspruch 20, worin die eindeutigen Marker Haptene beinhalten und worin jedes eindeutige Hapten sich von jedem anderen eindeutigen Hapten unterscheidet.
23. Verfahren nach Anspruch 20, worin die eindeutigen Marker spezifische Hybridisierungs sonden enthalten.
24. Verfahren nach Anspruch 22, worin das eindeutige Hapten verwendet wird, um die verschiedenen reorganisierten Moleküle zu trennen.
25. Verfahren nach Anspruch 24, worin die Trennung erreicht wird, indem ein spezifischer Bindungspartner für jedes eindeutige Hapten an einer unterschiedlichen Stelle auf einer festen Phase immobilisiert wird.
26. Verfahren nach Anspruch 24, worin die Trennung erreicht wird indem ein spezifischer Bindungspartner für jedes eindeutige Hapten auf einer festen Phase immobilisiert wird, und die feste Phase charakterisiert ist durch eine Eigenschaft, die die Unterscheidung voneinander gestattet.

Revendications

1. Procédé pour réaliser une amplification en chaîne par ligase multiplex comprenant les étapes suivantes :
 - a. fournir une solution réactionnelle contenant un acide nucléique d'un échantillon sous forme d'acide nucléique simple brin, ledit échantillon étant supposé avoir une ou plusieurs séquences d'acide nucléique cibles parmi une pluralité de séquences d'acide nucléique cibles ;
 - b. pour chaque séquence cible supposée, fournir dans la solution réactionnelle au moins quatre sondes d'acide nucléique (un ensemble de sondes), où: i) la première et la seconde desdites sondes sont des sondes primaires, et la troisième et la quatrième desdites sondes sont des sondes d'acide nucléique secondaires; ii) la première sonde est un simple brin qui s'hybride à un premier segment d'un brin primaire de l'acide nucléique cible ; iii) la seconde sonde est un simple brin qui s'hybride à un second segment dudit brin primaire de l'acide nucléique cible ; iv) l'extrémité 5' du premier segment dudit brin primaire de la cible est positionnée par rapport à l'extrémité 3' du second segment dudit brin primaire de la cible pour permettre la jonction de la première sonde à la seconde sonde quand lesdites sondes sont hybridées audit brin primaire dudit acide nucléique cible, en formant ainsi une molécule primaire réorganisée ayant une première partie et une seconde partie; v) la troisième sonde s'hybride à une première partie de la molécule primaire réorganisée; et vi) la quatrième sonde s'hybride à une seconde partie de la molécule primaire réorganisée, la première partie de la molécule primaire réorganisée étant positionnée par rapport à la seconde partie de la molécule primaire réorganisée pour permettre la jonction de la troisième sonde à la quatrième sonde quand lesdites troisième et quatrième sondes sont hybridées à ladite molécule primaire réorganisée, en formant ainsi une molécule secondaire réorganisée ; et

où, pour chaque séquence cible supposée, ledit ensemble de sondes est équilibré de manière que chaque ensemble de sondes soit fourni à une concentration qui permet ladite jonction en présence de chacun des autres ensembles de sondes ; et

où chaque ensemble de sondes produit un produit détectable après le même nombre de cycles d'amplification ; et

c. répéter le cycle suivant :

i) hybrider lesdites sondes à l'acide nucléique dans ledit échantillon;

ii) réaliser ladite jonction pour former lesdites molécules réorganisées ; et

iii) dénaturer l'acide nucléique dans ledit échantillon ;

de sorte que, avec des cycles successifs, la quantité de molécules primaires et secondaires réorganisées est augmentée pour chaque séquence cible supposée présente dans la solution réactionnelle.

2. Procédé selon la revendication 1 où ladite jonction est réalisée par une enzyme ligase, ou une enzyme ligase et une enzyme polymérase.

3. Procédé selon la revendication 1 où le cycle de l'étape c est répété de 20 à environ 60 fois.

4. Procédé selon la revendication 1 où au moins une sonde de chaque ensemble de sondes porte un marqueur détectable, chacun desdits marqueurs détectables pouvant être distingué des autres.

5. Procédé selon la revendication 4 où lesdits marqueurs détectables comprennent des haptènes qui peut être distingués sur la base de la spécificité de différents membres de liaison spécifique.

6. Procédé selon la revendication 1 où chacun des ensembles de sondes est marqué avec deux marqueurs distincts de sorte que, quand elles sont hybridées ensemble, les molécules réorganisées sont marquées avec deux marqueurs dont l'un au moins est un marqueur unique qui est différent pour chacun des ensembles de sondes.

7. Procédé selon la revendication 6 où l'autre marqueur est un marqueur commun, le même pour chaque ensemble de sondes.

8. Procédé selon la revendication 7 où le marqueur commun est utilisé pour la détection et est choisi dans le groupe consistant en les radio-isotopes, les fluorophores, les chimiluminophores et les haptènes.

9. Procédé selon la revendication 6 où les marqueurs uniques comprennent des membres de liaison spécifique uniques tels que chaque membre de liaison spécifique unique peut être distingué de tous les autres membres de liaison spécifique.

10. Procédé selon la revendication 9 où les marqueurs uniques comprennent des haptènes spécifiques.

11. Procédé selon la revendication 9 où les marqueurs uniques comprennent des sondes d'hybridation spécifiques.

12. Procédé selon la revendication 9 où le membre de liaison spécifique unique est utilisé pour séparer les molécules réorganisées d'un ensemble de sondes des molécules réorganisées d'au moins un autre ensemble de sondes.

13. Procédé selon la revendication 12 où la séparation est réalisée par immobilisation d'un partenaire de liaison spécifique pour chaque membre de liaison spécifique à un emplacement différent sur une phase solide.

14. Procédé selon la revendication 12 où la séparation est réalisée par immobilisation d'un partenaire de liaison spécifique pour chaque membre de liaison spécifique sur une phase solide, ladite phase solide étant caractérisée par une propriété qui permet de les distinguer les uns des autres.

15. Procédé de détection de la présence, de l'absence ou de la quantité de chaque séquence d'acide nucléique cible parmi une pluralité de séquences d'acide nucléique cibles par une amplification en chaîne par ligase multiplex comprenant les étapes suivantes :

a. fournir une solution réactionnelle contenant un acide nucléique d'un échantillon sous forme d'acide nucléi-

que simple brin, ledit échantillon étant supposé avoir une ou plusieurs séquences d'acide nucléique cibles parmi une pluralité de séquences d'acide nucléique cibles ;

- 5 b. pour chaque séquence cible supposée, fournir dans la solution réactionnelle un ensemble d'au moins deux et éventuellement de quatre sondes d'acide nucléique (un ensemble de sondes), où: i) la première et la seconde desdites sondes sont des sondes primaires, et la troisième et la quatrième éventuelles desdites sondes sont des sondes d'acide nucléique secondaires; ii) la première sonde est un simple brin qui s'hybride à un premier segment d'un brin primaire de l'acide nucléique cible; iii) la seconde sonde est un simple brin qui s'hybride à un second segment dudit brin primaire de l'acide nucléique cible; iv) l'extrémité 5' du premier segment dudit brin primaire de la cible est positionnée par rapport à l'extrémité 3' du second segment dudit brin primaire de la cible pour permettre la jonction de la première sonde à la seconde sonde quand lesdites sondes sont hybridées audit brin primaire dudit acide nucléique cible, en formant ainsi une molécule primaire réorganisée ayant une première partie et une seconde partie; v) la troisième sonde s'hybride à une première partie de la molécule primaire réorganisée; et vi) la quatrième sonde s'hybride à une seconde partie de la molécule primaire réorganisée, la première partie de la molécule primaire réorganisée étant positionnée par rapport à la seconde partie de la molécule primaire réorganisée pour permettre la jonction de la troisième sonde à la quatrième sonde quand lesdites troisième et quatrième sondes sont hybridées à ladite molécule primaire réorganisée, en formant ainsi une molécule secondaire réorganisée ;
- 10 où au moins une sonde de chaque ensemble de sondes contient un marqueur détectable, le marqueur détectable associé à chaque ensemble de sondes pouvant être distingué des marqueurs détectables associés aux autres ensembles de sondes, de sorte que la présence, l'absence ou la quantité de chaque séquence cible supposée peut être déterminée ; et
- 15 où, pour chaque séquence cible supposée, ledit ensemble de sondes est équilibré de manière que chaque ensemble de sondes soit fourni à une concentration qui permet ladite jonction en présence de chacun des autres ensembles de sondes ; et
- 20 où chaque ensemble de sondes produit un produit détectable après le même nombre de cycles d'amplification ; et
- 25 c. réaliser le cycle suivant :

- 30 i) hybrider lesdites sondes avec l'acide nucléique dans ledit échantillon ;
 ii) réaliser ladite jonction pour former lesdites molécules réorganisées ; et
 iii) dénaturer l'acide nucléique dans ledit échantillon ;

de sorte que, avec chaque cycle, la quantité de molécules primaires et, éventuellement, secondaires réorganisées est augmentée pour chaque séquence cible supposée présente dans la solution réactionnelle ; et

35 d. mesurer le marqueur détectable associé à chacun desdits ensembles de sondes à titre de mesure de la présence ou de la quantité d'acide nucléique cible dans la solution réactionnelle.

16. Procédé selon la revendication 15 où ladite jonction est réalisée par une enzyme ligase, ou une enzyme ligase et une enzyme polymérase.
- 40 17. Procédé selon la revendication 15 où lesdites troisième et quatrième sondes sont fournies et le cycle de l'étape c est répété de 10 à environ 100 fois.
18. Procédé selon la revendication 15 où le cycle de l'étape c est répété de 20 à environ 60 fois.
- 45 19. Procédé selon la revendication 15 où les sondes sont marquées avec deux marqueurs de sorte que les molécules réorganisées sont marquées avec deux marqueurs dont l'un au moins est un marqueur unique qui est différent pour chacun des ensembles de sondes.
- 50 20. Procédé selon la revendication 17 où les sondes sont marquées avec deux marqueurs de sorte que les molécules réorganisées sont marquées avec deux marqueurs dont l'un au moins est un marqueur unique qui est différent pour chacun des ensembles de sondes et l'autre est un marqueur commun.
21. Procédé selon la revendication 20 où le marqueur commun est utilisé pour la détection et est choisi dans le groupe consistant en les radio-isotopes, les fluorophores, les chimiluminophores et les haptènes.
- 55 22. Procédé selon la revendication 20 où les marqueurs uniques comprennent des haptènes et où chaque haptène unique diffère de tous les autres haptènes uniques.

23. Procédé selon la revendication 20 où les marqueurs uniques comprennent des sondes d'hybridation spécifiques.

24. Procédé selon la revendication 22 où l'haptène unique est utilisé pour séparer les différentes molécules réorganisées.

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25. Procédé selon la revendication 24 où la séparation est réalisée par immobilisation d'un partenaire de liaison spécifique pour chaque haptène unique à un emplacement différent sur une phase solide.

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26. Procédé selon la revendication 24 où la séparation est réalisée par immobilisation d'un partenaire de liaison spécifique pour chaque haptène unique sur une phase solide, ladite phase solide étant caractérisée par une propriété qui permet de les distinguer les uns des autres.

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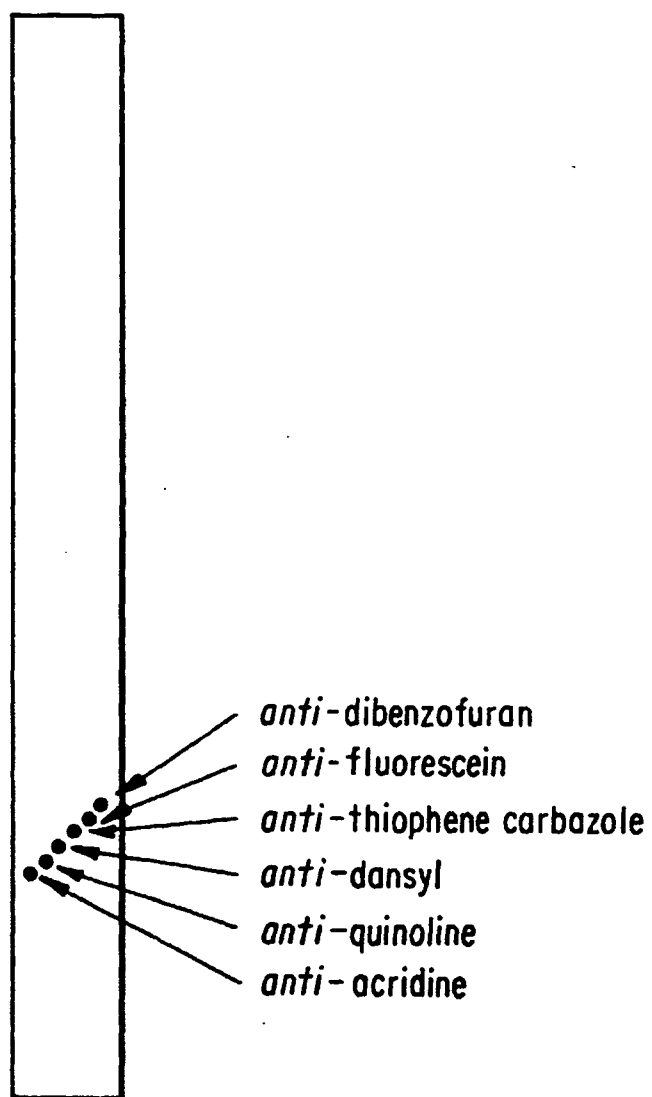


FIG. 1

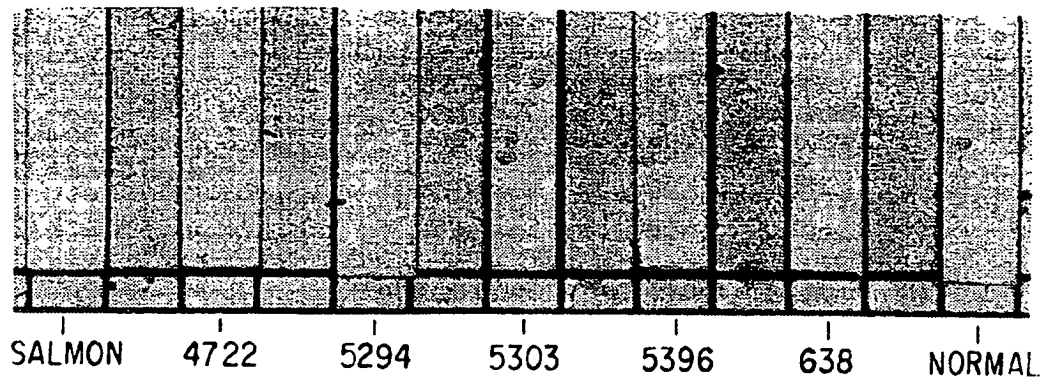


FIG. 2a

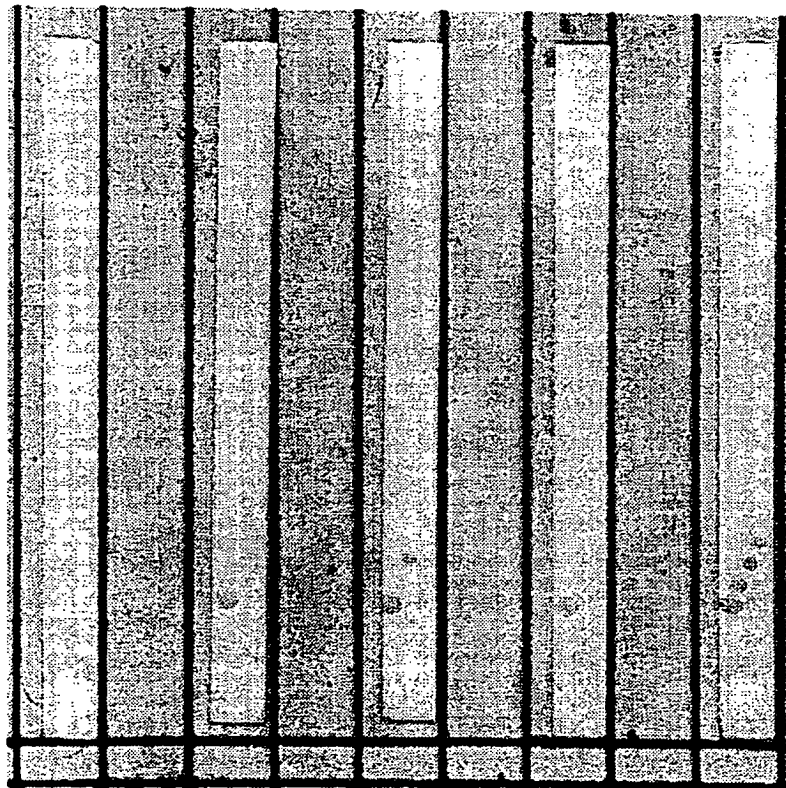


FIG. 2b

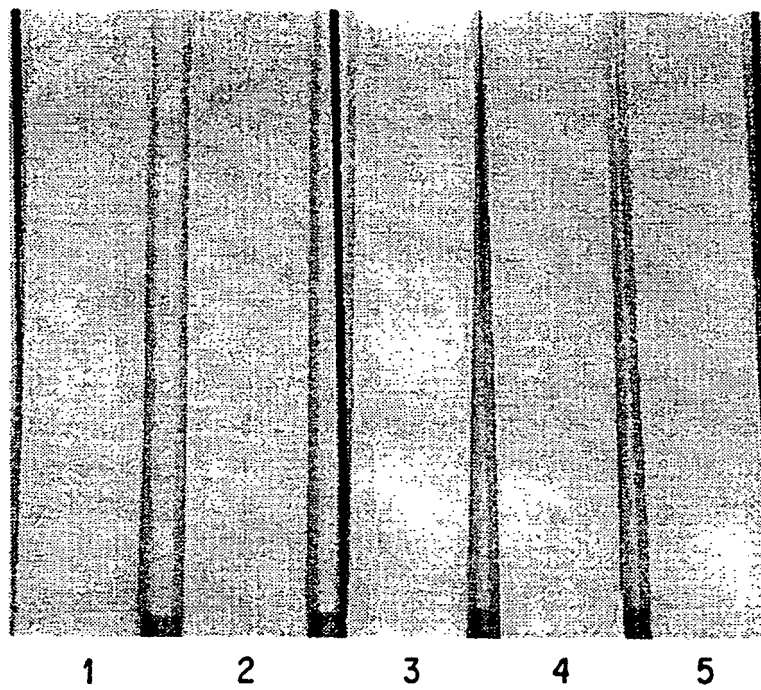


FIG. 3